

DB 241 LRLAKNRYLVLEANPNFVLPHTLHDADAILLVYGGKALMKIHRDNRESYNLECGDVI 300
QY LRLAKNRYLVLEANPNFVLPHTLHDADAILLVYGGKALMKIHRDNRESYNLECGDVI 300
DB 301 RIRAGTFFYLINDNNRHLIAKFILOTISTPGQYKEFFPAGGONPEPYLSTFSKEILEEA 360
QY RIRAGTFFYLINDNNRHLIAKFILOTISTPGQYKEFFPAGGONPEPYLSTFSKEILEEA 360
DB 361 LNTQTERLRLGVGLGOQREGVYIRASQEQIRLRLTRDSDSRMHIRRGESSRGPYNLFNKR 420
QY 361 LNTQTERLRLGVGLGOQREGVYIRASQEQIRLRLTRDSDSRMHIRRGESSRGPYNLFNKR 420
DB 421 PLYSNKYGAYEVKPEPDYRQLQDMVSVFIANTTQSGMGPFFNTSTKYVVAASGEADV 480
QY 421 PLYSNKYGAYEVKPEPDYRQLQDMVSVFIANTTQSGMGPFFNTSTKYVVAASGEADV 480
DB 481 EMACPHLSGRHGRGGKRRHEEEDVHYEQVRAKLSKRAIYVLAGHPYVFGSSGNENLL 540
QY 481 EMACPHLSGRHGRGGKRRHEEEDVHYEQVRAKLSKRAIYVLAGHPYVFGSSGNENLL 540
DB 541 LFAFGINAQNNHNFVLAGRERNVLOQIEPQAMELAFASRKEVEELFNSODESIFFPGR 600
QY 541 LFAFGINAQNNHNFVLAGRERNVLOQIEPQAMELAFASRKEVEELFNSODESIFFPGR 600
DB 601 QHQOQSPRSTKQOQPLVSLIDVGF 625
QY 601 QHQOQSPRSTKQOQPLVSLIDVGF 625

RESULT 2

ID W62828 standard; Protein: 666 AA.
AC W62828;
DT 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..666
FT /note= "mature protein"
PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB: V42311.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1, Page 39-41; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 666 AA;

Query Match 97.1%; Score 4496; DB 1; Length 666;
Best Local Similarity 96.6%; Pred. No. 0.00e+00;
Matches 604; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
DB 42 QCMQLETSGMRRCVSCQDKRFEEDIDMSKYNDQDDPOTDCQOCQRCRQOESGPRQOY 101
QY 1 QCMQLETSGMRRCVSCQDKRFEEDIDMSKYNDQDDPOTDCQOCQRCRQOESDPRQOY 60
DB 102 CORCKEICEEEEEYNNRQDPQOYEQCCORCRHETEPHNMOTCOQRCERYEKKRQ 161
QY 61 CORCKEICEEEEEYNNRQDPQOYEQCCORCRHETEPHNMOTCOQRCERYEKKRQ 120
DB 162 OKRYEEOQREDEKYEERKKEEONKRDPOQREYEDCRRCEQOEPQOYOCQRCREQR 221
QY 121 OKRYEEOQREDEKYEERKKEEONKRDPOQREYEDCRRCEQOEPQOYOCQRCREQR 180

DB 222 QHGRGDLINPORGSGRGYEEGEKOSDNPPYFDEKSLSTRTERGHISVLENYGRSK 281
QY 181 QHGRGDLINPORGSGRGYEEGEKOSDNPPYFDEKSLSTRTERGHISVLENYGRSK 240
DB 282 LRLAKNRYLVLEANPNFVLPHTLHDADAILLVYGGKALMKIHRDNRESYNLECGDVI 341
QY 241 LRLAKNRYLVLEANPNFVLPHTLHDADAILLVYGGKALMKIHRDNRESYNLECGDVI 300
DB 342 RIRAGTFFYLINDNNRHLIAKFILOTISTPGQYKEFFPAGGONPEPYLSTFSKEILEEA 401
QY 301 RIRAGTFFYLINDNNRHLIAKFILOTISTPGQYKEFFPAGGONPEPYLSTFSKEILEEA 360
DB 402 LNTQTERLRLGVGLGOQREGVYIRASQEQIRLRLTRDSDSRMHIRRGESSRGPYNLFNKR 461
QY 361 LNTQTERLRLGVGLGOQREGVYIRASQEQIRLRLTRDSDSRMHIRRGESSRGPYNLFNKR 420
DB 462 PLYSNKYGAYEVKPEPDYRQLQDMVSVFIANTTQSGMGPFFNTSTKYVVAASGEADV 521
QY 421 PLYSNKYGAYEVKPEPDYRQLQDMVSVFIANTTQSGMGPFFNTSTKYVVAASGEADV 480
DB 522 EMACPHLSGRHGRGGKRRHEEEDVHYEQVRAKLSKRAIYVLAGHPYVFGSSGNENLL 581
QY 481 EMACPHLSGRHGRGGKRRHEEEDVHYEQVRAKLSKRAIYVLAGHPYVFGSSGNENLL 540
DB 582 LFAFGINAQNNHNFVLAGRERNVLOQIEPQAMELAFASRKEVEELFNSODESIFFPGR 641
QY 541 LFAFGINAQNNHNFVLAGRERNVLOQIEPQAMELAFASRKEVEELFNSODESIFFPGR 600
DB 642 QHQOQSPRSTKQOQPLVSLIDVGF 666
QY 601 QHQOQSPRSTKQOQPLVSLIDVGF 625

RESULT 3

ID W62828 standard; Protein: 666 AA.
AC W62828;
DT 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..666
FT /note= "mature protein"
PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB: V42310.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1, Page 34-36; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 666 AA;

Query Match 96.9%; Score 4487; DB 1; Length 666;
Best Local Similarity 96.6%; Pred. No. 0.00e+00;
Matches 604; Conservative 11; Mismatches 8; Indels 0; Gaps 0;
DB 42 QCMQLETSGMRRCVSCQDKRFEEDIDMSKYNDQDDPOTDCQOCQRCRQOESGPRQOY 101
QY 1 QCMQLETSGMRRCVSCQDKRFEEDIDMSKYNDQDDPOTDCQOCQRCRQOESDPRQOY 60
DB 102 CORCKEICEEEEEYNNRQDPQOYEQCCORCRHETEPHNMOTCOQRCERYEKKRQ 161
QY 61 CORCKEICEEEEEYNNRQDPQOYEQCCORCRHETEPHNMOTCOQRCERYEKKRQ 120

442 ODMVSVFIANTIGSGMGPFFNTRSTKVYVVASGEADVEMACPHLSGRHGGGGRHE 501
Db KSSPS-YHRISDDLKPGWVFPVPGHPVTYIASNKENLIMICEVANRDNK-KTFPAGD 455
OY 502 EEEVHYEVRARLSKREAIIVLAGHPVYVSSGNNLLFFAFGINAONNHENF-LAGNE 560
Db 456 -NIVSSLDNVAKEAFNYPSEMVNGVF 481
OY 561 RNVLOQIEPOMELAFPAASRKEVEELF 587
RESULT 10
ID W62838 standard; protein: 605 AA.
AC W62838;
DT 27-OCT-1998 (first entry)
DE Glycine max antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Glycine max.
PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (REIR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JT, Manners JM, Marcus JP;
DR WPI: 98-37729/32.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
useful for controlling microbial infestations of plants or mammals
PT Claim 1: Page 63-65; 96pp: English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 605 AA:
Query Match 21.0%; Score 972; DB 1; Length 605;
Best Local Similarity 32.8%; Pred. No. 7,08e-75;
Matches 194; Conservative 162; Mismatches 194; Indels 41; Gaps 32;
Db 38 CLQSC-NSESDSYRNQACHARNLKEKECEGEIIPRR-PRQHP-EREPPQGEKE 94
OY 44 CORRCROESDPRQOYQCRCKEICEEEYNRQDRPOQYEQCRQCRRETEPRHM 103
Db 95 EDEDE-QPR-PIPPRPPQR-QEEHEORE-QEWP RK-EERKGEKSEED-EDEDEQ 148
OY 104 ICQQCERREYERKRRQOQRYEQREDEKYEERKEDNDRDPOQREYECRRHCEQ 163
Db 149 DER-OFPPRPAPHOKERNEEDEDQOQRESEES-EDSELRRKNNKPFELGSRNFTL 206
OY 164 EERLQYQORQROEOORHGRGDLMPORGSGRYEGE-EKQSD-NPYTFDESLSTR 221
Db 207 FKNQYGRIVLQRFNORSFQNLNDYRILEFNSKPNLLPNNADADYLVILNGTAL 266
OY 222 FRTGEGHISVLENFYGRSLRLALKNYRLVLEAPNAEVLPTHDADAIIIVIGRGAL 281
Db 267 SLVNNDDDSYLOGSDALRVPSGTTYYVNNNDNNELRLITLAPVYKPGFESEFELS 326
OY 282 KHIHNDNRSYVLECGDVIRIPAGTFYILINDNNEERLHIAFLQITISPGGYKKEFFPAG 341
Db 327 TPAQOQSYLOGFNRILIEASDYTKFEEINKVLFRESGOQOQGEORLOESYVIEISQORA 386
OY 342 GONPEPLYSTFKEKLEALNTO-TE--R-L--R--GV-L-GQOR--EGYTIASQOIRE 390
Db 387 LSKRAKSSSRK-TI--SSED-K-PNLRSRDPISYKSLKFEIPEKPNQDRDDIFLS 441
OY 391 LT-RDSESRRHIRRGSGSRGPNLFRKRLPLYSNKYGOAEVYKPEDYRQLQDMDSVF 449
Db 442 IVDNMEGALLPHFNSKALVILYINEGDANIELV-G-LKEQOQEO---QOEOPLEVR-- 494
OY 450 IANITQSGSMGPFNTRSKVYVVASGEADVEMACPHLSGRHGGGGRHEEEVHYE 509
Db 495 KRAIETSEODIVIPAGYVYV-VNATS-NLNFPAIGAINAONNRNLASQONVISOIPS 552
OY 510 OVRARLSKREAIIVLAGHPVYVSSGNNLLFPAGINONNHENFLAGREKNVILQIEP 569

553 QVQELAFPGSAQAVEKLKNGRESYFVDAQPKKKEGNKGRG--PLSSIL 601
Db 570 QAMELAFASRKREVELEFNSQDESIFFFGPRHQOQSPRSTKQOQPLVSIL 620
OY
RESULT 11
ID W90340 standard; protein: 444 AA.
AC W90340;
DT 24-MAY-1999 (first entry)
DE G. max truncated SBP1 protein.
KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
KW seed; carbohydrate content; soybean.
OS Glycine max.
PN W09853086-A1.
PD 26-NOV-1998.
PF 21-MAY-1998; U10465.
PR 22-MAY-1997; US-047568.
PA (UNITW) UNIV WASHINGTON STATE RES FOUND.
PI Chao WS, Grimes HD;
DR WPI: 99-070155/06.
PT New modified plant; sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds
PS Claim 7; Page 36-37; 38pp: English.
CC This sequence represents a novel sucrose binding protein, SBP1 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
SQ Sequence 444 AA;
Query Match 20.2%; Score 934; DB 1; Length 444;
Best Local Similarity 38.2%; Pred. No. 2.13e-71;
Matches 156; Conservative 112; Mismatches 121; Indels 19; Gaps 17;
Db 49 OQOQYTEDSKRVCIQSCDRHYRMKQER-EKQIQETRRKKEESREREEQ-EQHEE-Q 105
OY 149 QQREY-EDCRHHCQOEPRLOQOCRCQEQORQHGRG-DLMPORGSGRYEGEERQ 206
Db 106 DENPIFEEDKDFEYRVTEGGRIVLKFKTEKSKLQIGENFRALIDEARAFVSPRH 165
OY 207 SDNPYTFDE-KSLSTRFTEGHSVLENFYGRSKLRLAKNRYLVLEAPNAFVLP 265
Db 166 FDSEVVEFNIGRAVLGLVSESETEKTLLEPGDMIHIPAGTPLYIVNDENDKFLAMLH 225
OY 266 LDADAIIIVIGRGALKMHIHNDNRSYVLECGDVIRIPAGTFYILINDNNEERLHIAKF- 324
Db 226 IPVSYSTGKFEFEFFAPGRPEVSLSFWMVYQALQOTKGLNVFDQONGSIFRI 285
OY 325 LO-TISTPGQYKEFFPAGQNPDEPLSTFSKEILEALNTOETRLRGVLOQORGVYIRA 383
Db 286 SREOYRALAPTKKSSM-WPF--GGES-KPQENISKRPTISNGYGRLEVEGPDDEKSWL 341
OY 384 SQEQIRELTRDSESRKHHIRRGSGSRGPNLFRKRLPLYSNKYGOAEVYKPEDY-RQ-L 441
Db 442 QRLNMLTFTITORSNSTIYNSHAKIALVIDRGHLQISCPHMSR-SSHS--R-HD 397
OY 442 ODMVSVFIANTIGSGMGPFFNTRSTKVYVVASGEADVEMACPHLSGRHGGGGRHE 501
Db 398 KSSPS-YHRISDDLKPGWVFPVPGHPVTYIASNKENLIMICEVANR 444
OY 502 EEEVHYEVRARLSKREAIIVLAGHPVYVSSGNNLLFPAGINNO 549

ID	RESULT	12
AC	W22150	standard; protein; 626 AA.
DB	W22150	standard; protein; 626 AA.
DT	29-DEC-1997	(first entry)
DE	Peanut allergen Ara hi.	
KW	Peanut; seed storage protein; allergen; allergy; hypersensitivity;	
KW	vaccine; anaphylactic shock; immunotherapy; therapy;	
KW	monoclonal antibody; ELISA; analysis; Ara hi.	
OS	Archis hypogaea strain Floturner.	
EH	Key	Location/Qualifiers
FT	Peptide	1..22
FT	Protein	/label= Sig.peptide
FT	Modified_site	23..626
FT		/label= Mat.protein
FT		521..523
FT		/note= "N-glycosylation site"
PN	MO9724139-A1.	
PD	10-JUL-1997.	
PF	23-SEP-1996.	U15222.
PR	04-MAR-1996.	US-610424.
PR	29-DEC-1995.	US-009455.
PA	(UTAR-) UNIV ARKANSAS.	
PI	Bannon GA, Burks AW, Cockrell G, Helm RM, Stanley JS;	
PI	WPI: 97-363453/33.	
DR	N-PSDB: T76613.	
PT	Peanut allergens Ara hi and Ara hII - used for vaccination and in	
PT	two-site monoclonal antibody based ELISA	
PS	Claim 31; Page 172; 354pp.	
CC	This polypeptide comprises mofor peanut allergen Ara hi (W22149).	
CC	its sequence was deduced from cDNA clone p41b (T76613), isolated	
CC	from peanut seed cDNA using a primer (see T76616) based on an	
CC	isolated Ara hi peptide (see W24206). The sequence shows	
CC	significant homology with the vicilin family of seed storage	
CC	proteins of other legumes. The allergen is recognised by serum	
CC	IGE from a large proportion of individuals with peanut	
CC	hypersensitivity. Ara hi and Ara hII (see W24164) can be used to	
CC	raise monoclonal antibodies which are used in a specific two-site	
CC	Map ELISA for the detection of Ara hi or Ara hII (claimed). IGE-	
CC	binding Ara hi antigen epitopes (see W24165-87) may be used in	
CC	vaccines to protect against allergic reactions to peanut allergens,	
CC	e.g. anaphylactic shock.	
SQ	Sequence 626 AA;	
	Query Match	19.9%; Score 920; DB 1; Length 626;
	Best Local Similarity	33.6%; Pred. No. 4.06e-70;
	Matches 190; Conservative 153; Mismatches 185; Indels 38; Gaps 26;	
DB	47	QOEPPDLKOKACESCCTLEYEDPCVYDPRGHTTQNSRSPGERTR-GROPGYDDRR 105
OY	78	ORDPQOYQYQ-CQKRCQRETERPHNMOCCQRCRERYEKERKQKXYEQRE-DEKY 135
DB	106	QPRREEGS-RMGAPGRE-RE-REE-DWRODREDMR--RPSHOQPKRIKRGREGQEWG 159
OY	136	EEKMEKGNKRDPQ-OREYEDCRHCEQOEPRLYOCORCOEQOOROHGRGDDLPNPG 194
DB	160	TGSGIVR-EELSRRNPFFFSRRSTRGNGNGRIYVQRFDOSSRFOQNRIYQIE 218
OY	195	GSGRYEESGKQSDPIYFEDRSITRETEGHIVLENYGSKILRLAKKNRLVLE 254
DB	219	AKPNTLVPRKADADNLIVIOGQATVAVANGNNRKSNNLDEGHALIPSGFISYILNRH 278
OY	255	ANPNAFVLFTHLDAILLVIGGAGALKMIRHNRRESVNLGCGVIRIIPAGTFTYLLNRD 314
DB	279	DNQNLRAVKISMVYTPQGEPDFEPASSRDOSSTYLQGSRNTEPAFNAEFNEIRVLE 338
OY	315	NNERLHIKPFLOTISTPQYKEFPFAPAGQONDEPYLSTFSKEILAAANTQERLRGVL- 372
DB	339	ENAGGEQEEERQRRMSTPSSNNNGVIVKYVKEHVEELTKAKSVKSGSEEDINPI 398
OY	373	-----GQNE-CVT--IRASQ-Q-IHELTRDD-SE-SRR-WHI-RRGE--SS-RGPY 414

D	b		399	NLGEEDLSNNEKLFEEVDPDKNKQLODDMLTCVCIKGALPLPFENSKAVIVV	458
O	y		415	NLEKKRLPYISKNKGQAVEVPED-YKOLODMVSVFIANTITGSMMGPFFNRSTRKVVV	473
D	b		459	NKGTNLELVAVRKEOQGRREEDEDEEBSGNREVRRTARLKEGDVFIMPAHPV	518
O	y		474	ASGDVADEM-ACPHLSRGHRGGRRKHEEBEEVHYEQY---ARLSKREALVLVAGHV	529
D	b		519	A-INASSE-LHLGFGTNAENHRIPLAGDKONVIDQIEKAOKADLPFSGSGOVERKLIN	576
O	y		530	VFSSGNGENILLFAFGINAQNHNENFLAGRERWVLOQIOPAMELAFAASRKREVELEFN	589
D	b		577	QKESHFYSAHQOSQSSPSSPEKESP	602
O	y		590	QDESIFFPGRHOQOSPSTKQOP	615
R	E	S	U	L	T
I	D		13		
A	C		WT0342	standard; protein; 409 AA.	
D	T		WT0342;		
D	E		24-MAY-1999	(first entry)	
K	M		G.	max truncated SBP2 protein.	
K	M		SBP1;	sucrose binding protein; SBP2;	sucrose uptake; transgenic plant;
K	M		seed;	carbohydrate content; soybean.	
O	S		Glycine max.		
P	N		WT0835086-AI.		
P	D		26-NOV-1998.		
P	F		21-MAY-1998;	U10465.	
P	R		22-MAY-1997;	US-047568.	
P	A		(UNIW.)	UNIV WASHINGTON STATE RES FOUND.	
P	I		Chao WS,	Grimes HD.	
D	R		WP1:	99-070155/06.	
P	T		New modified plant	sucrose binding proteins - used to develop	
P	T		transgenic plants	which can have enhanced or decreased sucrose	
P	T		uptake activity	in developing seeds	
P	S		Claim 7:	Page 39-40; 58pp: English.	
C	C		This sequence represents	a novel sucrose binding protein, SBP2 isolated	
C	C		from Glycine max.	This protein is used in a method resulting in the	
C	C		production of a modified plant	sucrose binding protein (SBP) which has a	
C	C		modified amino acid sequence compared to	a corresponding wild-type SBP,	
C	C		and where expression of the modified SBP	in a yeast assay system confers	
C	C		enhanced sucrose uptake compared to the	corresponding wild-type SBP.	
C	C		The products of the invention can be used	for producing transgenic plants	
C	C		which have modified sucrose uptake activity,	particularly in developing	
C	C		seeds. Enhanced sucrose uptake activity	in developing seeds may be	
C	C		desirable where it is an advantage	to increase the carbohydrate content	
C	C		of the seed (e.g. where the seed is the	primary plant material harvested	
C	C		such as soybean). In contrast,	decreased sucrose uptake activity in	
C	C		seeds might be desirable where the	vegetative material of the plant is	
C	C		harvested. The SBP regulatory regions	confers specific or enhanced	
C	C		expression in developing seeds and so	may be used to express any	
C	C		transgene in developing seeds.		
S	Q		Sequence	409 AA:	
Q	U		Query Match	19.6%;	Score 907;
B	e		Best local Similarity	38.8%;	Pred. No. 6, 27e-69;
M	a		Matches 137;	Conservative 102;	Mismatches 100;
I	n			Indels 14;	Gaps 12;
D	b		35	EDPLVLYCKHQCOOO--R-QYTSDMKRTLCQQCDMSKKOREQOVEEFETREKEFHQBONE	91
O	y		149	QQRVEDCRRHCOCDEPRLOY-QCCOR-C-OE-QQRHOGRGDDLNNPORGSGRYEEG-E	203
D	b		92	EEDDENNYVEEKDESTRVTECGSIRYLKFKTERSKLOGIENFRLLAEAFRAHFVS	151
O	y		204	EKGSDNRYTYDE-RSLSTRTRTEGHISTVLNFNTGYSKILRLKRYRLVLEANNNAVYL	262
D	b		152	PRHDSFVLNLKIGRAVLGLVNSETEKITLEPGDMIHIPAGTPPLYIVNRDENKLLA	211
O	y		263	PTHLDADAAILLVIGRGVALKMHIRDRRESYNLEGGVIRIPAGTFEYLINRDNNERTLIA	322
D	b		212	MHLPIVTSPEKFEDEFPGRGPDSEVLSAFSNMNVLOALQTPKGLERLRFNQONGSIFK	271
O	y		323	KFLQDTISPPQYEVEPAGQONPEPLTSFSKEILEEALANTETELRGVLGOORGVIIIR	382

ID	Accession	Protein	Score	DB	Length	Query Match
Db	272	ISRRFRLATPKTKSSW-WPF--GGES-KAOFNIFSKRPTFSNGYLTEWGPDEDESKL	19.4%	33.8%	614	Best Local Similarity
Qy	383	ASQOIRLTLDSEDSRRMWHIRGESSRGYNLFNRRPLXSNKYGAYEKKPEPDYQ-L	157	175	42	Matches
Db	328	QRLNMLTFTNITQSRKSTIHYNSHAKIALVMDRGHLQISCPHMSRSDSK	19.4%	33.8%	614	Best Local Similarity
Qy	442	ODMVSVFIANITQGSMMGPFNTRSTFRTKVVVAVSGEADVEMACPRLSGRHGR	157	175	42	Matches
RESULT	14	W22149 standard; protein; 614 AA.				
AC	W22149	29-DEC-1997 (first entry)				
DT	29-DEC-1997	(first entry)				
DE	Peanut allergen Ara hi.					
KW	Peanut; seed storage protein; allergen; allergy; hypersensitivity;					
KW	vaccine; anaphylactic shock; immunotherapy; therapy;					
KW	monoclonal antibody; ELISA; analysis; Ara hi.					
OS	Arachis hypogaea strain Florunner.					
FS	Key	Location/Qualifier				
FT	Peptide	1..22				
FT	/label= Sig_peptide					
FT	Protein	23..614				
FT	/label= Mat_protein					
FT	Modified_site	521..523				
FT	/note= "N-glycosylation site"					
PN	W09724139-A1.					
PD	10-JUL-1997.					
PF	23-SEP-1996; U15222.					
PR	04-MAR-1996; US-610424.					
PR	29-DEC-1995; US-009455.					
PA	(UYAR)- UNIV ARKANSAS.					
PI	Bannon GA, Burks AW, Cockrell G, Helm RM, Stanley JS;					
DR	WPI; 97-363453/33.					
DR	N-PSDB: T76612.					
PT	Peanut allergens Ara hi and Ara hii - used for vaccination and in					
PS	two-site monoclonal antibody based ELISA					
PT	Claim 31: Page 169: 354pp: English.					
CC	This polypeptide comprises major peanut allergen Ara hi (W22149).					
CC	Its sequence was deduced from cDNA clone P17 (T76612), isolated					
CC	from peanut seed cDNA using a primer (see T76612) based on an					
CC	isolated Ara hi peptide (see W24206). The sequence shows					
CC	significant homology with the vicilin family of seed storage					
CC	proteins of other legumes. The allergen is recognised by serum					
CC	IgE from a large proportion of individuals with peanut					
CC	hypersensitivity. Ara hi and Ara hii (see W24164) can be used to					
CC	raise monoclonal antibodies which are used in a specific two-site					
CC	Mab ELISA for the detection of Ara hi or Ara hii (claimed). IGE-					
CC	binding Ara hi antigen epitopes (see W24165-87) may be used in					
CC	vaccines to protect against allergic reactions to peanut allergens,					
CC	e.g. anaphylactic shock.					
CC	Sequence 614 AA:					
SO	Query Match	19.4%	Score 897;	DB 1;	Length 614;	
	Best Local Similarity	33.8%	Pred. No. 5.13e-68;			
	Matches 191;	Conservative 157;	Mismatches 175;	Indels 42;	Gaps 28;	

[illegible]

